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SEQUENCE LISTING

<110> GRONER, BERND
MORITZ, DIRK

<120> BIFUNCTIONAL PROTEIN, PREPARATION AND USE

<130> 24741-1521

<140> 09/596,774

<141> 2000-06-19

<150> 09/159,027

<151> 1998-09-23

<150> 08/793,048

<151> 1996-11-01

<150> PCT/EP95/01494

<151> 1995-04-20

<150> EP 94810244.7

<151> 1994-05-02

<160> 16

<170> PatentIn Ver. 3.2

<210> 1

<211> 748

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
chimeric nucleotide sequence

<220>

<221> CDS

<222> (9)..(728)

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Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Lys Lys Pro
1 5 10

gga gag aca gtc aag atc tcc tgc aag gcc tct ggg tat cct ttc aca 98
Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Pro Phe Thr
15 20 25 30

aac tat gga atg aac tgg gtg aag cag gct cca gga cag ggt tta aag 146
Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Lys
35 40 45

tgg atg ggc tgg att aac act tcc act gga gag tca aca ttt gct gat	194
Trp Met Gly Trp Ile Asn Thr Ser Thr Gly Glu Ser Thr Phe Ala Asp	
50 55 60	
gac ttc aag gga cgg ttt gac ttc tct ttg gaa acc tct gcc aac act	242
Asp Phe Lys Gly Arg Phe Asp Phe Ser Leu Glu Thr Ser Ala Asn Thr	
65 70 75	
gcc tat ttg cag atc aac aac ctc aaa agt gaa gac atg gct aca tat	290
Ala Tyr Leu Gln Ile Asn Asn Leu Lys Ser Glu Asp Met Ala Thr Tyr	
80 85 90	
ttc tgt gca aga tgg gag gtt tac cac ggc tac gtt cct tac tgg ggc	338
Phe Cys Ala Arg Trp Glu Val Tyr His Gly Tyr Val Pro Tyr Trp Gly	
95 100 105 110	
caa ggg acc acg gtc acc gtt tcc tct ggc ggt ggc ggt tct ggt ggc	386
Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly	
115 120 125	
ggt ggc tcc ggc ggt ggc ggt tct gac atc cag ctg acc cag tct cac	434
Gly Gly Ser Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser His	
130 135 140	
aaa ttc ctg tcc act tca gta gga gac agg gtc agc atc acc tgc aag	482
Lys Phe Leu Ser Thr Ser Val Gly Asp Arg Val Ser Ile Thr Cys Lys	
145 150 155	
gcc agt cag gat gtg tat aat gct gtt gcc tgg tat caa cag aaa cca	530
Ala Ser Gln Asp Val Tyr Asn Ala Val Ala Trp Tyr Gln Gln Lys Pro	
160 165 170	
gga caa tct cct aaa ctt ctg att tac tcg gca tcc tcc cgg tac act	578
Gly Gln Ser Pro Lys Leu Leu Ile Tyr Ser Ala Ser Ser Arg Tyr Thr	
175 180 185 190	
gga gtc cct tct cgc ttc act ggc agt ggc tct ggg ccg gat ttc act	626
Gly Val Pro Ser Arg Phe Thr Gly Ser Gly Ser Gly Pro Asp Phe Thr	
195 200 205	
ttc acc atc agc agt gtg cag gct gaa gac ctg gca gtt tat ttc tgt	674
Phe Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Phe Cys	
210 215 220	
cag caa cat ttt cgt act cca ttc acg ttc ggc tcg ggg aca aaa ttg	722
Gln Gln His Phe Arg Thr Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu	
225 230 235	
gag atc tagctgatca aagctctaga	748
Glu Ile	
240	

<210> 2
 <211> 240
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 chimeric amino acid sequence

<400> 2

Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu	Lys	Lys	Pro	Gly	Glu	1	5	10	15
Thr	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Pro	Phe	Thr	Asn	Tyr	20	25	30	
Gly	Met	Asn	Trp	Val	Lys	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Lys	Trp	Met	35	40	45	
Gly	Trp	Ile	Asn	Thr	Ser	Thr	Gly	Glu	Ser	Thr	Phe	Ala	Asp	Asp	Phe	50	55	60	
Lys	Gly	Arg	Phe	Asp	Phe	Ser	Leu	Glu	Thr	Ser	Ala	Asn	Thr	Ala	Tyr	65	70	75	80
Leu	Gln	Ile	Asn	Asn	Leu	Lys	Ser	Glu	Asp	Met	Ala	Thr	Tyr	Phe	Cys	85	90	95	
Ala	Arg	Trp	Glu	Val	Tyr	His	Gly	Tyr	Val	Pro	Tyr	Trp	Gly	Gln	Gly	100	105	110	
Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	115	120	125	
Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Gln	Leu	Thr	Gln	Ser	His	Lys	Phe	130	135	140	
Leu	Ser	Thr	Ser	Val	Gly	Asp	Arg	Val	Ser	Ile	Thr	Cys	Lys	Ala	Ser	145	150	155	160
Gln	Asp	Val	Tyr	Asn	Ala	Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	165	170	175	
Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Ser	Ala	Ser	Ser	Arg	Tyr	Thr	Gly	Val	180	185	190	
Pro	Ser	Arg	Phe	Thr	Gly	Ser	Gly	Ser	Gly	Pro	Asp	Phe	Thr	Phe	Thr	195	200	205	
Ile	Ser	Ser	Val	Gln	Ala	Glu	Asp	Leu	Ala	Val	Tyr	Phe	Cys	Gln	Gln	210	215	220	
His	Phe	Arg	Thr	Pro	Phe	Thr	Phe	Gly	Ser	Gly	Thr	Lys	Leu	Glu	Ile	225	230	235	240

<210> 3
 <211> 748
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 chimeric nucleotide sequence

<220>
 <221> CDS
 <222> (9)..(728)

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 Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro
 1 5 10

ggg act tca gtg aag ctg tcc tgc aag gct tct gat tac acc ttc acc 98
 Gly Thr Ser Val Lys Leu Ser Cys Lys Ala Ser Asp Tyr Thr Phe Thr
 15 20 25 30

agc tac tgg atg aac tgg gtg aag cag agg cct gga caa ggc ctt gaa 146
 Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu
 35 40 45

tgg att ggt atg att gat cct tca gac agt gaa act caa tac aat caa 194
 Trp Ile Gly Met Ile Asp Pro Ser Asp Ser Glu Thr Gln Tyr Asn Gln
 50 55 60

atg ttc aag gac aag gcc gca ttg act gta gac aag tcc tcc aat aca 242
 Met Phe Lys Asp Lys Ala Ala Leu Thr Val Asp Lys Ser Ser Asn Thr
 65 70 75

gcc tac atg caa ctc agc agc ctg aca tct gag gac tct gcg gtc tat 290
 Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr
 80 85 90

tac tgt gca aaa ggg ggg gcc tct ggg gac tgg tac ttc gat gtc tgg 338
 Tyr Cys Ala Lys Gly Gly Ala Ser Gly Asp Trp Tyr Phe Asp Val Trp
 95 100 105 110

ggc caa ggg acc acg gtc acc gtt tcc tct ggc ggt ggc ggt tct ggt 386
 Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
 115 120 125

ggc ggt ggc tcc ggc ggt ggc ggt tct gac atc cag ctg acc cag tct 434
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser
 130 135 140

cca tcc tca ctg tct gca tct ctg gga ggc gaa gtc acc atc act tgc 482
Pro Ser Ser Leu Ser Ala Ser Leu Gly Gly Glu Val Thr Ile Thr Cys
145 150 155

aag gca agc caa gac att aag aag tat ata gct tgg tac caa cac aag 530
Lys Ala Ser Gln Asp Ile Lys Lys Tyr Ile Ala Trp Tyr Gln His Lys
160 165 170

cct gga aaa agt cct cgg cta ctc ata cac tac aca tct gta tta cag 578
Pro Gly Lys Ser Pro Arg Leu Leu Ile His Tyr Thr Ser Val Leu Gln
175 180 185 190

cca ggc atc cca tcc agg ttc agt gga agt ggg tct ggg aga gat tat 626
Pro Gly Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Arg Asp Tyr
195 200 205

tcc ttc agc atc cac aac ctg gag cct gaa gat att gca act tat tat 674
Ser Phe Ser Ile His Asn Leu Glu Pro Glu Asp Ile Ala Thr Tyr Tyr
210 215 220

tgt cta cat tat gat tat ctg tac acg ttc gga ggg ggc acc aag ctg 722
Cys Leu His Tyr Asp Tyr Leu Tyr Thr Phe Gly Gly Gly Thr Lys Leu
225 230 235

gag atc tagctgatca aagctctaga 748
Glu Ile
240

<210> 4

<211> 240

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
chimeric amino acid sequence

<400> 4

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Thr
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Asp Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Met Ile Asp Pro Ser Asp Ser Glu Thr Gln Tyr Asn Gln Met Phe
50 55 60

Lys Asp Lys Ala Ala Leu Thr Val Asp Lys Ser Ser Asn Thr Ala Tyr
65 70 75 80

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<210> 5
<211> 1479
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic
chimeric nucleotide sequence

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<222> (40) .. (1422)
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<400> 5
gaattcggca cgagcttaag gcaccatttc ttagacatc atg gct tgg gtg tgg      54
                                     Met Ala Trp Val Trp
                                     1           5

acc ttg cta ttc ctg atg gca gct gcc aaa gtg ccc aag cag atc cag      102
Thr Leu Leu Phe Leu Met Ala Ala Ala Lys Val Pro Lys Gln Ile Gln
          10                15                20

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ttg gtg cag tct gga cct gag ctg aag aag cct gga gag aca gtc aag	150
Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu Thr Val Lys	
25 30 35	
atc tcc tgc aag gcc tct ggg tat cct ttc aca aac tat gga atg aac	198
Ile Ser Cys Lys Ala Ser Gly Tyr Pro Phe Thr Asn Tyr Gly Met Asn	
40 45 50	
tgg gtg aag cag gct cca gga cag ggt tta aag tgg atg ggc tgg att	246
Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Lys Trp Met Gly Trp Ile	
55 60 65	
aac acc tcc act gga gag tca aca ttt gct gat gac ttc aag gga cgg	294
Asn Thr Ser Thr Gly Glu Ser Thr Phe Ala Asp Asp Phe Lys Gly Arg	
70 75 80 85	
ttt gac ttc tct ttg gaa acc tct gcc aac act gcc tat ttg cag atc	342
Phe Asp Phe Ser Leu Glu Thr Ser Ala Asn Thr Ala Tyr Leu Gln Ile	
90 95 100	
aac aac ctc aaa agt gaa gac atg gct aca tat ttc tgt gca aga tgg	390
Asn Asn Leu Lys Ser Glu Asp Met Ala Thr Tyr Phe Cys Ala Arg Trp	
105 110 115	
gag gtt tac cac ggc tac gtt cct tac tgg ggc caa ggg acc acg gtc	438
Glu Val Tyr His Gly Tyr Val Pro Tyr Trp Gly Gln Gly Thr Thr Val	
120 125 130	
acc gtt tcc tct ggc ggt ggc ggt tct ggt ggc ggt ggc tcc ggc ggt	486
Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly	
135 140 145	
ggc ggt tct gac atc cag ctg acc cag tct cac aaa ttc ctg tcc act	534
Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser His Lys Phe Leu Ser Thr	
150 155 160 165	
tca gta gga gac agg gtc agc atc acc tgc aag gcc agt cag gat gtg	582
Ser Val Gly Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val	
170 175 180	
tat aat gct gtt gcc tgg tat caa cag aaa cca gga caa tct cct aaa	630
Tyr Asn Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys	
185 190 195	
ctt ctg att tac tcg gca tcc tcc cgg tac act gga gtc cct tct cgc	678
Leu Leu Ile Tyr Ser Ala Ser Ser Arg Tyr Thr Gly Val Pro Ser Arg	
200 205 210	
ttc act ggc agt ggc tct ggg ccg gat ttc act ttc acc atc agc agt	726
Phe Thr Gly Ser Gly Ser Gly Pro Asp Phe Thr Phe Thr Ile Ser Ser	
215 220 225	

gtg cag gct gaa gac ctg gca gtt tat ttc tgt cag caa cat ttt cgt Val Gln Ala Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln His Phe Arg 230 235 240 245	774
act cca ttc acg ttc ggc tcg ggg aca aaa ttg gag atc aaa gct cta Thr Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Ala Leu 250 255 260	822
gag atc agc aac tcg gtg atg tac ttc agt tct gtc gtg cca gtc ctt Glu Ile Ser Asn Ser Val Met Tyr Phe Ser Ser Val Val Pro Val Leu 265 270 275	870
cag aaa gtg aac tct act act acc aag cca gtg ctg cga act ccc tca Gln Lys Val Asn Ser Thr Thr Thr Lys Pro Val Leu Arg Thr Pro Ser 280 285 290	918
cct gtg cac cct acc ggg aca tct cag ccc cag aga cca gaa gat tgt Pro Val His Pro Thr Gly Thr Ser Gln Pro Gln Arg Pro Glu Asp Cys 295 300 305	966
cgg ccc cgt ggc tca gtg aag ggg acc gga ttg gac ttt cta gag gat Arg Pro Arg Gly Ser Val Lys Gly Thr Gly Leu Asp Phe Leu Glu Asp 310 315 320 325	1014
ccc aaa ctc tgc tac ttg cta gat gga atc ctc ttc atc tac gga gtc Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu Phe Ile Tyr Gly Val 330 335 340	1062
atc atc aca gcc ctg tac ctg aga gca aaa ttc agc agg agt gca gag Ile Ile Thr Ala Leu Tyr Leu Arg Ala Lys Phe Ser Arg Ser Ala Glu 345 350 355	1110
act gct gcc aac ctg cag gac ccc aac cag ctc tac aat gag ctc aat Thr Ala Ala Asn Leu Gln Asp Pro Asn Gln Leu Tyr Asn Glu Leu Asn 360 365 370	1158
cta ggg cga aga gag gaa tat gac gtc ttg gag aag aag cgg gct cgg Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Glu Lys Lys Arg Ala Arg 375 380 385	1206
gat cca gag atg gga ggc aaa cag cag agg agg agg aac ccc cag gaa Asp Pro Glu Met Gly Gly Lys Gln Gln Arg Arg Arg Asn Pro Gln Glu 390 395 400 405	1254
ggc gta tac aat gca ctg cag aaa gac aag atg gca gaa gcc tac agt Gly Val Tyr Asn Ala Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser 410 415 420	1302
gag atc ggc aca aaa ggc gag agg cgg aga ggc aag ggg cac gat ggc Glu Ile Gly Thr Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly 425 430 435	1350

ctt tac cag ggt ctc agc act gcc acc aag gac acc tat gat gcc ctg 1398
Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
440 445 450

cat atg cag acc ctg gcc cct cgc taacagccag ggcattttctc cctcacgggc 1452
His Met Gln Thr Leu Ala Pro Arg
455 460

agatccccgg gtaccgagct cgaattc 1479

<210> 6

<211> 461

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic chimeric amino acid sequence

<400> 6

Met Ala Trp Val Trp Thr Leu Leu Phe Leu Met Ala Ala Ala Lys Val
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Pro Lys Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro
20 25 30

Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Pro Phe Thr .
35 40 45

Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Lys
50 55 60

Trp Met Gly Trp Ile Asn Thr Ser Thr Gly Glu Ser Thr Phe Ala Asp
65 70 75 80

Asp Phe Lys Gly Arg Phe Asp Phe Ser Leu Glu Thr Ser Ala Asn Thr
85 90 95

Ala Tyr Leu Gln Ile Asn Asn Leu Lys Ser Glu Asp Met Ala Thr Tyr
100 105 110

Phe Cys Ala Arg Trp Glu Val Tyr His Gly Tyr Val Pro Tyr Trp Gly
115 120 125

Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser His
145 150 155 160

Lys Phe Leu Ser Thr Ser Val Gly Asp Arg Val Ser Ile Thr Cys Lys
165 170 175

Ala Ser Gln Asp Val Tyr Asn Ala Val Ala Trp Tyr Gln Gln Lys Pro
 180 185 190
 Gly Gln Ser Pro Lys Leu Leu Ile Tyr Ser Ala Ser Ser Arg Tyr Thr
 195 200 205
 Gly Val Pro Ser Arg Phe Thr Gly Ser Gly Ser Gly Pro Asp Phe Thr
 210 215 220
 Phe Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Phe Cys
 225 230 235 240
 Gln Gln His Phe Arg Thr Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu
 245 250 255
 Glu Ile Lys Ala Leu Glu Ile Ser Asn Ser Val Met Tyr Phe Ser Ser
 260 265 270
 Val Val Pro Val Leu Gln Lys Val Asn Ser Thr Thr Thr Lys Pro Val
 275 280 285
 Leu Arg Thr Pro Ser Pro Val His Pro Thr Gly Thr Ser Gln Pro Gln
 290 295 300
 Arg Pro Glu Asp Cys Arg Pro Arg Gly Ser Val Lys Gly Thr Gly Leu
 305 310 315 320
 Asp Phe Leu Glu Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu
 325 330 335
 Phe Ile Tyr Gly Val Ile Ile Thr Ala Leu Tyr Leu Arg Ala Lys Phe
 340 345 350
 Ser Arg Ser Ala Glu Thr Ala Ala Asn Leu Gln Asp Pro Asn Gln Leu
 355 360 365
 Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Glu
 370 375 380
 Lys Lys Arg Ala Arg Asp Pro Glu Met Gly Gly Lys Gln Gln Arg Arg
 385 390 395 400
 Arg Asn Pro Gln Glu Gly Val Tyr Asn Ala Leu Gln Lys Asp Lys Met
 405 410 415
 Ala Glu Ala Tyr Ser Glu Ile Gly Thr Lys Gly Glu Arg Arg Arg Gly
 420 425 430
 Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
 435 440 445
 Thr Tyr Asp Ala Leu His Met Gln Thr Leu Ala Pro Arg
 450 455 460

<210> 7
 <211> 443
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 chimeric amino acid sequence

<400> 7
 Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
 1 5 10 15
 Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Pro Phe Thr Asn Tyr
 20 25 30
 Gly Met Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Lys Trp Met
 35 40 45
 Gly Trp Ile Asn Thr Ser Thr Gly Glu Ser Thr Phe Ala Asp Asp Phe
 50 55 60
 Lys Gly Arg Phe Asp Phe Ser Leu Glu Thr Ser Ala Asn Thr Ala Tyr
 65 70 75 80
 Leu Gln Ile Asn Asn Leu Lys Ser Glu Asp Met Ala Thr Tyr Phe Cys
 85 90 95
 Ala Arg Trp Glu Val Tyr His Gly Tyr Val Pro Tyr Trp Gly Gln Gly
 100 105 110
 Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 115 120 125
 Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser His Lys Phe
 130 135 140
 Leu Ser Thr Ser Val Gly Asp Arg Val Ser Ile Thr Cys Lys Ala Ser
 145 150 155 160
 Gln Asp Val Tyr Asn Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 165 170 175
 Ser Pro Lys Leu Leu Ile Tyr Ser Ala Ser Ser Arg Tyr Thr Gly Val
 180 185 190
 Pro Ser Arg Phe Thr Gly Ser Gly Ser Gly Pro Asp Phe Thr Phe Thr
 195 200 205
 Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln
 210 215 220

His Phe Arg Thr Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile
 225 230 235 240
 Lys Ala Leu Glu Ile Ser Asn Ser Val Met Tyr Phe Ser Ser Val Val
 245 250 255
 Pro Val Leu Gln Lys Val Asn Ser Thr Thr Thr Lys Pro Val Leu Arg
 260 265 270
 Thr Pro Ser Pro Val His Pro Thr Gly Thr Ser Gln Pro Gln Arg Pro
 275 280 285
 Glu Asp Cys Arg Pro Arg Gly Ser Val Lys Gly Thr Gly Leu Asp Phe
 290 295 300
 Leu Glu Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu Phe Ile
 305 310 315 320
 Tyr Gly Val Ile Ile Thr Ala Leu Tyr Leu Arg Ala Lys Phe Ser Arg
 325 330 335
 Ser Ala Glu Thr Ala Ala Asn Leu Gln Asp Pro Asn Gln Leu Tyr Asn
 340 345 350
 Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Glu Lys Lys
 355 360 365
 Arg Ala Arg Asp Pro Glu Met Gly Gly Lys Gln Gln Arg Arg Arg Asn
 370 375 380
 Pro Gln Glu Gly Val Tyr Asn Ala Leu Gln Lys Asp Lys Met Ala Glu
 385 390 395 400
 Ala Tyr Ser Glu Ile Gly Thr Lys Gly Glu Arg Arg Arg Gly Lys Gly
 405 410 415
 His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
 420 425 430
 Asp Ala Leu His Met Gln Thr Leu Ala Pro Arg
 435 440

<210> 8

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 8

ctgaaagctt agatctgccc gtgagggaga aatgcctgg c

<210> 9
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 9
 tcgatctaga aagtccaatc cggccccctt cactg 35

<210> 10
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 10
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<210> 11
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 11
 tcgatctaga gatcagcaac tcggtgatgt acttcag 37

<210> 12
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 linker peptide

<400> 12
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1 5 10 15

<210> 13
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 13
 agcttctaga gtttcagagc acagctctca cggcc 35

<210> 14
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 14
 tcgatctaga gtctggttca cccctctgg 29

<210> 15
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 15
 Glu Ile Lys Ala Leu Glu Ile Ser Asn Ser
 1 5 10

<210> 16
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 16
 Gly Leu Asp Phe Leu Glu Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly
 1 5 10 15